* * * * * * * * * * Welcome to STN International * * * * * * * * * *

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NEWS 4 JAN 26 Improved Timeliness of CAS Indexing Adds Value to USPATFULL and USPAT2 Chemistry Patents
NEWS 5 JAN 26 Updated MeSH vocabulary, new structured abstracts, and other enhancements improve searching in STN reload of MEDLINE
NEWS 6 JAN 28 CABA will be updated weekly
NEWS 7 FEB 23 PCTFULL file on STN completely reloaded
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NEWS 9 FEB 25 LPCI will be replaced by LDPCI
NEWS 10 MAR 07 Pricing for SELECTing Patent, Application, and Priority Numbers in the USPAT and IFI Databases Families is Now Consistent with Similar Patent Databases on STN
NEWS 11 APR 26 Expanded Swedish Patent Application Coverage in CA/CAplus Provides More Current and Complete Information
NEWS 12 APR 28 The DWPI (files WPINDEX, WPIDS and WPIX) on STN have been enhanced with thesauri for the European Patent Classifications
NEWS 13 MAY 02 MEDLINE Improvements Provide Fast and Simple Access to DOI and Chemical Name Information
NEWS 14 MAY 12 European Patent Classification thesauri added to the INPADOC files, PCTFULL, GBFULL and FRFULL
NEWS 15 MAY 23 Enhanced performance of STN biosequence searches
NEWS 16 MAY 23 Free Trial of the Numeric Property Search Feature in PCTFULL on STN
NEWS 17 JUN 20 STN on the Web Enhanced with New Patent Family Assistant and Updated Structure Plug-In
NEWS 18 JUN 20 INPADOC databases enhanced with first page images
NEWS 19 JUN 20 PATDPA database updates to end in June 2011
NEWS 20 JUN 26 MARPAT Enhancements Save Time and Increase Usability
NEWS 21 JUL 25 STN adds Australian patent full-text database, AUPATFULL, including the new numeric search feature.
NEWS 22 AUG 01 CA Sections Added to ACS Publications Web Editions Platform
NEWS 23 AUG 16 INPADOC: Coverage of German Patent Data resumed, enhanced legal status
NEWS 24 AUG 18 Upgrade now to STN Express, Version 8.5
NEWS 25 SEP 01 CAS Journal Coverage Now Includes Ahead-of-Print Articles for More Than 100 Journal Titles
NEWS 26 SEP 01 Older Versions of STN Express to be Discontinued Beginning in March 2012
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FILE 'HOME' ENTERED AT 16:32:16 ON 25 SEP 2011

=> s (ybl056w or ydr149c or ylr285w or ylr311c or yor331c or ypr123c or ydr525w? or ydr539w)/bi,ab
THIS COMMAND NOT AVAILABLE IN THE CURRENT FILE
Some commands only work in certain files. For example, the EXPAND
command can only be used to look at the index in a file which has an
index. Enter "HELP COMMANDS" at an arrow prompt (=>) for a list of
commands which can be used in this file.

=> file caplus

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.69	0.69

FILE 'CAPLUS' ENTERED AT 16:34:05 ON 25 SEP 2011
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

FILE COVERS 1907 - 25 Sep 2011 VOL 155 ISS 14
FILE LAST UPDATED: 23 Sep 2011 (20110923/ED)
REVISED CLASS FIELDS (/NCL) LAST RELOADED: Jun 2011
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE: Jun 2011

CAplus now includes complete International Patent Classification (IPC)
reclassification data for the second quarter of 2011.

CAS Information Use Policies apply and are available at:

http://www.cas.org/legal/infopolicy.html

This file contains CAS Registry Numbers for easy and accurate
substance identification.

=> s (ykl?)/bi,ab
522 (YKL?)/BI
423 (YKL?)/AB
L1 522 (YKL?)/BI,AB

=> s (ybl056w or ydr149c or ylr285w or ylr311c)/bi,ab
2 YBL056W/BI
0 YBL056W/AB
5 YDR149C/BI
0 YDR149C/AB
1 YLR285W/BI
0 YLR285W/AB

```
             5 YLR311C/BI
             0 YLR311C/AB
L2           9 (YBL056W OR YDR149C OR YLR285W OR YLR311C)/BI,AB

=> s (yor331c or ypr123c or ydr525w? or ydr539w or ydr540c orygl246c or yjl204c)/bi,ab
             4 YOR331C/BI
             1 YOR331C/AB
             1 YPR123C/BI
             0 YPR123C/AB
             3 YDR525W?/BI
             1 YDR525W?/AB
             5 YDR539W/BI
             1 YDR539W/AB
             1 YDR540C/BI
             0 ORYGL246C/BI
             0 YDR540C ORYGL246C/BI
                 ((YDR540C(W)ORYGL246C)/BI)
             0 YDR540C/AB
             0 ORYGL246C/AB
             0 YDR540C ORYGL246C/AB
                 ((YDR540C(W)ORYGL246C)/AB)
             6 YJL204C/BI
             2 YJL204C/AB
L3          14 (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C ORYGL246C
               OR YJL204C)/BI,AB

=> s (ylr282c or ylr287c or ylr290c or yjl188c or yjl192c or yjl211c or ykl037w or ylr283w)/bi,ab
             2 YLR282C/BI
             0 YLR282C/AB
             2 YLR287C/BI
             0 YLR287C/AB
             3 YLR290C/BI
             0 YLR290C/AB
             3 YJL188C/BI
             0 YJL188C/AB
             1 YJL192C/BI
             0 YJL192C/AB
             4 YJL211C/BI
             0 YJL211C/AB
             2 YKL037W/BI
             1 YKL037W/AB
             1 YLR283W/BI
             0 YLR283W/AB
L4           9 (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL211C
               OR YKL037W OR YLR283W)/BI,AB

=> s (ylr312c or ylr315c or ylr320w ot ypl030w)/bi,ab
             4 YLR312C/BI
             0 YLR312C/AB
             0 YLR315C/BI
             0 YLR315C/AB
             3 YLR320W/BI
         12985 OT/BI
             2 YPL030W/BI
             0 YLR320W OT YPL030W/BI
                 ((YLR320W(W)OT(W)YPL030W)/BI)
             0 YLR320W/AB
         10522 OT/AB
             1 YPL030W/AB
             0 YLR320W OT YPL030W/AB
                 ((YLR320W(W)OT(W)YPL030W)/AB)
```

```
L5              4 (YLR312C OR YLR315C OR YLR320W OT YPL030W)/BI,AB

=> s (ykl080w or ylr447c or yhr06w or ypr036w or yhr039c? or yhr026w)/bi,ab
                1 YKL080W/BI
                0 YKL080W/AB
                1 YLR447C/BI
                0 YLR447C/AB
                0 YHR06W/BI
                0 YHR06W/AB
                2 YPR036W/BI
                0 YPR036W/AB
                4 YHR039C?/BI
                1 YHR039C?/AB
                2 YHR026W/BI
                0 YHR026W/AB
L6              6 (YKL080W OR YLR447C OR YHR06W OR YPR036W OR YHR039C? OR YHR026W)
                  /BI,AB

=> s (ygl026c or ygr180c or ydr127w or ycr028c or ylr284c or yor221c or yal021c or ygl224c)/bi,ab
                2 YGL026C/BI
                0 YGL026C/AB
                4 YGR180C/BI
                0 YGR180C/AB
                4 YDR127W/BI
                1 YDR127W/AB
                3 YCR028C/BI
                1 YCR028C/AB
                5 YLR284C/BI
                2 YLR284C/AB
                3 YOR221C/BI
                1 YOR221C/AB
                3 YAL021C/BI
                0 YAL021C/AB
                2 YGL224C/BI
                1 YGL224C/AB
L7             12 (YGL026C OR YGR180C OR YDR127W OR YCR028C OR YLR284C OR YOR221C
                  OR YAL021C OR YGL224C)/BI,AB

=> s (ybl042c or ydr148c or yhl025w or ylr307w or ylr345w or ylr354c ypl129w or ypr060c)/bi,ab
                3 YBL042C/BI
                2 YBL042C/AB
                2 YDR148C/BI
                0 YDR148C/AB
                2 YHL025W/BI
                0 YHL025W/AB
                3 YLR307W/BI
                0 YLR307W/AB
                5 YLR345W/BI
                1 YLR345W/AB
                3 YLR354C/BI
                2 YPL129W/BI
                1 YLR354C YPL129W/BI
                    ((YLR354C(W)YPL129W)/BI)
                0 YLR354C/AB
                0 YPL129W/AB
                0 YLR354C YPL129W/AB
                    ((YLR354C(W)YPL129W)/AB)
                2 YPR060C/BI
                1 YPR060C/AB
L8             10 (YBL042C OR YDR148C OR YHL025W OR YLR307W OR YLR345W OR YLR354C
                  YPL129W OR YPR060C)/BI,AB
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=> s (ygr180c or ydr150w or ygl240w ot ybl058w or yil036w or ylr226w or ylr381w or yor026w)/bi,ab
             4 YGR180C/BI
             0 YGR180C/AB
             3 YDR150W/BI
             1 YDR150W/AB
             3 YGL240W/BI
         12985 OT/BI
             3 YBL058W/BI
             0 YGL240W OT YBL058W/BI
                 ((YGL240W(W)OT(W)YBL058W)/BI)
             0 YGL240W/AB
         10522 OT/AB
             0 YBL058W/AB
             0 YGL240W OT YBL058W/AB
                 ((YGL240W(W)OT(W)YBL058W)/AB)
             2 YIL036W/BI
             0 YIL036W/AB
             4 YLR226W/BI
             0 YLR226W/AB
             6 YLR381W/BI
             0 YLR381W/AB
             3 YOR026W/BI
             0 YOR026W/AB
L9          12 (YGR180C OR YDR150W OR YGL240W OT YBL058W OR YIL036W OR YLR226W
               OR YLR381W OR YOR026W)/BI,AB

=> s (ypl018w or ybl063w or ydr363w? or yir026c or ylr234w or ymr032w or ypl129w)/bi,ab
             3 YPL018W/BI
             0 YPL018W/AB
             1 YBL063W/BI
             0 YBL063W/AB
             1 YDR363W?/BI
             0 YDR363W?/AB
             1 YIR026C/BI
             0 YIR026C/AB
             2 YLR234W/BI
             0 YLR234W/AB
             4 YMR032W/BI
             2 YMR032W/AB
             2 YPL129W/BI
             0 YPL129W/AB
L10          6 (YPL018W OR YBL063W OR YDR363W? OR YIR026C OR YLR234W OR YMR032W
               OR YPL129W)/BI,AB

=> s (ygr006w or yil036w or ykr082w or ylr226w or yml112w or ymr021c or yal021c or ydr195w or yol068c)/bi,ab
             2 YGR006W/BI
             0 YGR006W/AB
             2 YIL036W/BI
             0 YIL036W/AB
             3 YKR082W/BI
             1 YKR082W/AB
             4 YLR226W/BI
             0 YLR226W/AB
             4 YML112W/BI
             0 YML112W/AB
             2 YMR021C/BI
             0 YMR021C/AB
             3 YAL021C/BI
             0 YAL021C/AB
             2 YDR195W/BI
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             1 YDR195W/AB
             2 YOL068C/BI
             0 YOL068C/AB
L11          7 (YGR006W OR YIL036W OR YKR082W OR YLR226W OR YML112W OR YMR021C
               OR YAL021C OR YDR195W OR YOL068C)/BI,AB

=> s (ybr279w or ygl070c or ygl071w or ygl222c or yhl025w or ylr266c or ypl129w)/bi,ab
             2 YBR279W/BI
             0 YBR279W/AB
             2 YGL070C/BI
             0 YGL070C/AB
             1 YGL071W/BI
             0 YGL071W/AB
             1 YGL222C/BI
             0 YGL222C/AB
             2 YHL025W/BI
             0 YHL025W/AB
             6 YLR266C/BI
             1 YLR266C/AB
             2 YPL129W/BI
             0 YPL129W/AB
L12          7 (YBR279W OR YGL070C OR YGL071W OR YGL222C OR YHL025W OR YLR266C
               OR YPL129W)/BI,AB

=> s (ybl058w or ylr287c? or ygr0844c or ylr344w)/bi,ab
             3 YBL058W/BI
             0 YBL058W/AB
             2 YLR287C?/BI
             0 YLR287C?/AB
             0 YGR0844C/BI
             0 YGR0844C/AB
             1 YLR344W/BI
             0 YLR344W/AB
L13          4 (YBL058W OR YLR287C? OR YGR0844C OR YLR344W)/BI,AB

=> s (ykl080w or ylr447c or ygl240w or ygr105w or ygl206c)/bi,ab
             1 YKL080W/BI
             0 YKL080W/AB
             1 YLR447C/BI
             0 YLR447C/AB
             3 YGL240W/BI
             0 YGL240W/AB
             1 YGR105W/BI
             0 YGR105W/AB
             3 YGL206C/BI
             0 YGL206C/AB
L14          3 (YKL080W OR YLR447C OR YGL240W OR YGR105W OR YGL206C)/BI,AB

=> s (ykl119c or ydr414c or yhr060w or ylr292c or ylr306w or ygl227w or ygr270w)/bi,ab
             1 YKL119C/BI
             0 YKL119C/AB
             1 YDR414C/BI
             0 YDR414C/AB
             1 YHR060W/BI
             0 YHR060W/AB
             1 YLR292C/BI
             0 YLR292C/AB
             1 YLR306W/BI
             0 YLR306W/AB
             5 YGL227W/BI
             2 YGL227W/AB
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              4 YGR270W/BI
              1 YGR270W/AB
L15           6 (YKL119C OR YDR414C OR YHR060W OR YLR292C OR YLR306W OR YGL227W
                OR YGR270W)/BI,AB

=> s (ypr036w or ydr027c or yhr039c or ykl080w or ylr447c or ygl206c or ykr082w or ylr292c or ybl063w)/bi,ab
              2 YPR036W/BI
              0 YPR036W/AB
              2 YDR027C/BI
              1 YDR027C/AB
              4 YHR039C/BI
              1 YHR039C/AB
              1 YKL080W/BI
              0 YKL080W/AB
              1 YLR447C/BI
              0 YLR447C/AB
              3 YGL206C/BI
              0 YGL206C/AB
              3 YKR082W/BI
              1 YKR082W/AB
              1 YLR292C/BI
              0 YLR292C/AB
              1 YBL063W/BI
              0 YBL063W/AB
L16           10 (YPR036W OR YDR027C OR YHR039C OR YKL080W OR YLR447C OR YGL206C
                OR YKR082W OR YLR292C OR YBL063W)/BI,AB

=> s (yjr104c or ymr021c)/bi,ab
              3 YJR104C/BI
              0 YJR104C/AB
              2 YMR021C/BI
              0 YMR021C/AB
L17           3 (YJR104C OR YMR021C)/BI,AB

=> s (ypr036w or yhr039c? or ykl080w or ylr447c or ygl071w or yir026c)/bi,ab
              2 YPR036W/BI
              0 YPR036W/AB
              4 YHR039C?/BI
              1 YHR039C?/AB
              1 YKL080W/BI
              0 YKL080W/AB
              1 YLR447C/BI
              0 YLR447C/AB
              1 YGL071W/BI
              0 YGL071W/AB
              1 YIR026C/BI
              0 YIR026C/AB
L18           5 (YPR036W OR YHR039C? OR YKL080W OR YLR447C OR YGL071W OR YIR026C
                )/BI,AB

=> s (ydl151c or ybl058w)/bi,ab
              2 YDL151C/BI
              0 YDL151C/AB
              3 YBL058W/BI
              0 YBL058W/AB
L19           4 (YDL151C OR YBL058W)/BI,AB

=> s (ykr082w or ydl151c or yol068c or ydr363w? or yhl025w or yir026c or ylr307w or ymr032w or ypl129w)/bi,ab
              3 YKR082W/BI
              1 YKR082W/AB
              2 YDL151C/BI
```

```
                0 YDL151C/AB
                2 YOL068C/BI
                0 YOL068C/AB
                1 YDR363W?/BI
                0 YDR363W?/AB
                2 YHL025W/BI
                0 YHL025W/AB
                1 YIR026C/BI
                0 YIR026C/AB
                3 YLR307W/BI
                0 YLR307W/AB
                4 YMR032W/BI
                2 YMR032W/AB
                2 YPL129W/BI
                0 YPL129W/AB
L20             8 (YKR082W OR YDL151C OR YOL068C OR YDR363W? OR YHL025W OR YIR026C
                  OR YLR307W OR YMR032W OR YPL129W)/BI,AB

=> s (ydr027c or ydr414c or ylr381w orygr084c or ymr032w)/bi,ab
                2 YDR027C/BI
                1 YDR027C/AB
                1 YDR414C/BI
                0 YDR414C/AB
                6 YLR381W/BI
                0 ORYGR084C/BI
                0 YLR381W ORYGR084C/BI
                    ((YLR381W(W)ORYGR084C)/BI)
                0 YLR381W/AB
                0 ORYGR084C/AB
                0 YLR381W ORYGR084C/AB
                    ((YLR381W(W)ORYGR084C)/AB)
                4 YMR032W/BI
                2 YMR032W/AB
L21             5 (YDR027C OR YDR414C OR YLR381W ORYGR084C OR YMR032W)/BI,AB

=> s (ypr036w or yhr026w or yhr039c or ykl080w or ylr447c or ycr028c or ylr292c)/bi,ab
                2 YPR036W/BI
                0 YPR036W/AB
                2 YHR026W/BI
                0 YHR026W/AB
                4 YHR039C/BI
                1 YHR039C/AB
                1 YKL080W/BI
                0 YKL080W/AB
                1 YLR447C/BI
                0 YLR447C/AB
                3 YCR028C/BI
                1 YCR028C/AB
                1 YLR292C/BI
                0 YLR292C/AB
L22             8 (YPR036W OR YHR026W OR YHR039C OR YKL080W OR YLR447C OR YCR028C
                  OR YLR292C)/BI,AB

=> ybl056w/bi,ab
YBL056W IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s ybl056w/bi,ab
                2 YBL056W/BI
```

```
                0 YBL056W/AB
L23             2 YBL056W/BI,AB

=> s (ydr149c or ylr285w or ylr311c)/bi,ab
                5 YDR149C/BI
                0 YDR149C/AB
                1 YLR285W/BI
                0 YLR285W/AB
                5 YLR311C/BI
                0 YLR311C/AB
L24             9 (YDR149C OR YLR285W OR YLR311C)/BI,AB

=> s (yor331c or ypr123c or ydr525w? or ydr539w or ydr540c or ygl246c or yjl204c)/bi,ab
                4 YOR331C/BI
                1 YOR331C/AB
                1 YPR123C/BI
                0 YPR123C/AB
                3 YDR525W?/BI
                1 YDR525W?/AB
                5 YDR539W/BI
                1 YDR539W/AB
                1 YDR540C/BI
                0 YDR540C/AB
                3 YGL246C/BI
                1 YGL246C/AB
                6 YJL204C/BI
                2 YJL204C/AB
L25            16 (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C OR YGL246C
                   OR YJL204C)/BI,AB

=> s (ylr282c or ylr287c or ylr290c or yjl188c or yjl192c or yjl211c or ykl037w or ylr283w)/bi,ab
                2 YLR282C/BI
                0 YLR282C/AB
                2 YLR287C/BI
                0 YLR287C/AB
                3 YLR290C/BI
                0 YLR290C/AB
                3 YJL188C/BI
                0 YJL188C/AB
                1 YJL192C/BI
                0 YJL192C/AB
                4 YJL211C/BI
                0 YJL211C/AB
                2 YKL037W/BI
                1 YKL037W/AB
                1 YLR283W/BI
                0 YLR283W/AB
L26             9 (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL211C
                  OR YKL037W OR YLR283W)/BI,AB

=> s (ylr312c or ylr315w or ylr320w or ypl030w)/bi,ab
                4 YLR312C/BI
                0 YLR312C/AB
                2 YLR315W/BI
                0 YLR315W/AB
                3 YLR320W/BI
                0 YLR320W/AB
                2 YPL030W/BI
                1 YPL030W/AB
L27             7 (YLR312C OR YLR315W OR YLR320W OR YPL030W)/BI,AB
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=> d his

     (FILE 'HOME' ENTERED AT 16:32:16 ON 25 SEP 2011)

     FILE 'CAPLUS' ENTERED AT 16:34:05 ON 25 SEP 2011
L1            522 S (YKL?)/BI,AB
L2              9 S (YBL056W OR YDR149C OR YLR285W OR YLR311C)/BI,AB
L3             14 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C ORYGL24
L4              9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L5              4 S (YLR312C OR YLR315C OR YLR320W OT YPL030W)/BI,AB
L6              6 S (YKL080W OR YLR447C OR YHR06W OR YPR036W OR YHR039C? OR YHR02
L7             12 S (YGL026C OR YGR180C OR YDR127W OR YCR028C OR YLR284C OR YOR22
L8             10 S (YBL042C OR YDR148C OR YHL025W OR YLR307W OR YLR345W OR YLR35
L9             12 S (YGR180C OR YDR150W OR YGL240W OT YBL058W OR YIL036W OR YLR22
L10             6 S (YPL018W OR YBL063W OR YDR363W? OR YIR026C OR YLR234W OR YMR0
L11             7 S (YGR006W OR YIL036W OR YKR082W OR YLR226W OR YML112W OR YMR02
L12             7 S (YBR279W OR YGL070C OR YGL071W OR YGL222C OR YHL025W OR YLR26
L13             4 S (YBL058W OR YLR287C? OR YGR0844C OR YLR344W)/BI,AB
L14             3 S (YKL080W OR YLR447C OR YGL240W OR YGR105W OR YGL206C)/BI,AB
L15             6 S (YKL119C OR YDR414C OR YHR060W OR YLR292C OR YLR306W OR YGL22
L16            10 S (YPR036W OR YDR027C OR YHR039C OR YKL080W OR YLR447C OR YGL20
L17             3 S (YJR104C OR YMR021C)/BI,AB
L18             5 S (YPR036W OR YHR039C? OR YKL080W OR YLR447C OR YGL071W OR YIR0
L19             4 S (YDL151C OR YBL058W)/BI,AB
L20             8 S (YKR082W OR YDL151C OR YOL068C OR YDR363W? OR YHL025W OR YIR0
L21             5 S (YDR027C OR YDR414C OR YLR381W ORYGR084C OR YMR032W)/BI,AB
L22             8 S (YPR036W OR YHR026W OR YHR039C OR YKL080W OR YLR447C OR YCR02
L23             2 S YBL056W/BI,AB
L24             9 S (YDR149C OR YLR285W OR YLR311C)/BI,AB
L25            16 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C OR YGL2
L26             9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L27             7 S (YLR312C OR YLR315W OR YLR320W OR YPL030W)/BI,AB

=> s l2 or l3 or l4 or l5
L28            25 L2 OR L3 OR L4 OR L5

=> s l6 or l7 or l8 or l9 or l10
L29            27 L6 OR L7 OR L8 OR L9 OR L10

=> s l11 or l12 or l13 or l14 or l15
L30            13 L11 OR L12 OR L13 OR L14 OR L15

=> s l16 or l17 or l18 or l19 or l20
L31            13 L16 OR L17 OR L18 OR L19 OR L20

=> s l21 or l22 or l23 or l24 or l25 or l26 or l27
L32            34 L21 OR L22 OR L23 OR L24 OR L25 OR L26 OR L27

=> d his

     (FILE 'HOME' ENTERED AT 16:32:16 ON 25 SEP 2011)

     FILE 'CAPLUS' ENTERED AT 16:34:05 ON 25 SEP 2011
L1            522 S (YKL?)/BI,AB
L2              9 S (YBL056W OR YDR149C OR YLR285W OR YLR311C)/BI,AB
L3             14 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C ORYGL24
L4              9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L5              4 S (YLR312C OR YLR315C OR YLR320W OT YPL030W)/BI,AB
L6              6 S (YKL080W OR YLR447C OR YHR06W OR YPR036W OR YHR039C? OR YHR02
L7             12 S (YGL026C OR YGR180C OR YDR127W OR YCR028C OR YLR284C OR YOR22
L8             10 S (YBL042C OR YDR148C OR YHL025W OR YLR307W OR YLR345W OR YLR35
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L9          12 S (YGR180C OR YDR150W OR YGL240W OT YBL058W OR YIL036W OR YLR22
L10          6 S (YPL018W OR YBL063W OR YDR363W? OR YIR026C OR YLR234W OR YMR0
L11          7 S (YGR006W OR YIL036W OR YKR082W OR YLR226W OR YML112W OR YMR02
L12          7 S (YBR279W OR YGL070C OR YGL071W OR YGL222C OR YHL025W OR YLR26
L13          4 S (YBL058W OR YLR287C? OR YGR0844C OR YLR344W)/BI,AB
L14          3 S (YKL080W OR YLR447C OR YGL240W OR YGR105W OR YGL206C)/BI,AB
L15          6 S (YKL119C OR YDR414C OR YHR060W OR YLR292C OR YLR306W OR YGL22
L16         10 S (YPR036W OR YDR027C OR YHR039C OR YKL080W OR YLR447C OR YGL20
L17          3 S (YJR104C OR YMR021C)/BI,AB
L18          5 S (YPR036W OR YHR039C? OR YKL080W OR YLR447C OR YGL071W OR YIR0
L19          4 S (YDL151C OR YBL058W)/BI,AB
L20          8 S (YKR082W OR YDL151C OR YOL068C OR YDR363W? OR YHL025W OR YIR0
L21          5 S (YDR027C OR YDR414C OR YLR381W ORYGR084C OR YMR032W)/BI,AB
L22          8 S (YPR036W OR YHR026W OR YHR039C OR YKL080W OR YLR447C OR YCR02
L23          2 S YBL056W/BI,AB
L24          9 S (YDR149C OR YLR285W OR YLR311C)/BI,AB
L25         16 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C OR YGL2
L26          9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L27          7 S (YLR312C OR YLR315W OR YLR320W OR YPL030W)/BI,AB
L28         25 S L2 OR L3 OR L4 OR L5
L29         27 S L6 OR L7 OR L8 OR L9 OR L10
L30         13 S L11 OR L12 OR L13 OR L14 OR L15
L31         13 S L16 OR L17 OR L18 OR L19 OR L20
L32         34 S L21 OR L22 OR L23 OR L24 OR L25 OR L26 OR L27

=> s l28 or l29 or l30 or l31 or l32
L33         53 L28 OR L29 OR L30 OR L31 OR L32

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=> s l33 not 2011/py
        1404557 2011/PY
L34         50 L33 NOT 2011/PY

=> s l34 not 2010/py
        1963357 2010/PY
L35         43 L34 NOT 2010/PY

=> s l35 not 2009/py
        1917153 2009/PY
L36         42 L35 NOT 2009/PY

=> s l36 not 2008/py
        1812414 2008/PY
L37         37 L36 NOT 2008/PY

=> s l37 not 2007/py
        1731271 2007/PY
L38         36 L37 NOT 2007/PY

=> s l38 not 2006/py
        1592904 2006/PY
L39         33 L38 NOT 2006/PY

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        1437669 2005/PY
L40         30 L39 NOT 2005/PY

=> s l40 not 2004/py
        1355844 2004/PY
L41         24 L40 NOT 2004/PY
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=> d his

     (FILE 'HOME' ENTERED AT 16:32:16 ON 25 SEP 2011)

     FILE 'CAPLUS' ENTERED AT 16:34:05 ON 25 SEP 2011
L1          522 S (YKL?)/BI,AB
L2            9 S (YBL056W OR YDR149C OR YLR285W OR YLR311C)/BI,AB
L3           14 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C ORYGL24
L4            9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L5            4 S (YLR312C OR YLR315C OR YLR320W OT YPL030W)/BI,AB
L6            6 S (YKL080W OR YLR447C OR YHR06W OR YPR036W OR YHR039C? OR YHR02
L7           12 S (YGL026C OR YGR180C OR YDR127W OR YCR028C OR YLR284C OR YOR22
L8           10 S (YBL042C OR YDR148C OR YHL025W OR YLR307W OR YLR345W OR YLR35
L9           12 S (YGR180C OR YDR150W OR YGL240W OT YBL058W OR YIL036W OR YLR22
L10           6 S (YPL018W OR YBL063W OR YDR363W? OR YIR026C OR YLR234W OR YMR0
L11           7 S (YGR006W OR YIL036W OR YKR082W OR YLR226W OR YML112W OR YMR02
L12           7 S (YBR279W OR YGL070C OR YGL071W OR YGL222C OR YHL025W OR YLR26
L13           4 S (YBL058W OR YLR287C? OR YGR0844C OR YLR344W)/BI,AB
L14           3 S (YKL080W OR YLR447C OR YGL240W OR YGR105W OR YGL206C)/BI,AB
L15           6 S (YKL119C OR YDR414C OR YHR060W OR YLR292C OR YLR306W OR YGL22
L16          10 S (YPR036W OR YDR027C OR YHR039C OR YKL080W OR YLR447C OR YGL20
L17           3 S (YJR104C OR YMR021C)/BI,AB
L18           5 S (YPR036W OR YHR039C? OR YKL080W OR YLR447C OR YGL071W OR YIR0
L19           4 S (YDL151C OR YBL058W)/BI,AB
L20           8 S (YKR082W OR YDL151C OR YOL068C OR YDR363W? OR YHL025W OR YIR0
L21           5 S (YDR027C OR YDR414C OR YLR381W ORYGR084C OR YMR032W)/BI,AB
L22           8 S (YPR036W OR YHR026W OR YHR039C OR YKL080W OR YLR447C OR YCR02
L23           2 S YBL056W/BI,AB
L24           9 S (YDR149C OR YLR285W OR YLR311C)/BI,AB
L25          16 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C OR YGL2
L26           9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L27           7 S (YLR312C OR YLR315W OR YLR320W OR YPL030W)/BI,AB
L28          25 S L2 OR L3 OR L4 OR L5
L29          27 S L6 OR L7 OR L8 OR L9 OR L10
L30          13 S L11 OR L12 OR L13 OR L14 OR L15
L31          13 S L16 OR L17 OR L18 OR L19 OR L20
L32          34 S L21 OR L22 OR L23 OR L24 OR L25 OR L26 OR L27
L33          53 S L28 OR L29 OR L30 OR L31 OR L32
L34          50 S L33 NOT 2011/PY
L35          43 S L34 NOT 2010/PY
L36          42 S L35 NOT 2009/PY
L37          37 S L36 NOT 2008/PY
L38          36 S L37 NOT 2007/PY
L39          33 S L38 NOT 2006/PY
L40          30 S L39 NOT 2005/PY
L41          24 S L40 NOT 2004/PY

=> d l41 1-24 bib ab
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L41 ANSWER 1 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2004:63268 CAPLUS Full-text
DN 141:83397
TI Genetic control of recombination partner preference in yeast meiosis: isolation and characterization of mutants elevated for meiotic unequal sister-chromatid recombination. [Erratum to document cited in CA132:217873]
AU Thompson, Dawn A.; Stahl, Franklin W.
CS Institute of Molecular Biology, University of Oregon, Eugene, OR, 97403-1229, USA
SO Genetics (2003), 164(3), 1241
CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB A dmc1::LEU2 mutant was mislabeled and erroneously assigned to class II; the strain did not have the dominant meiotic lethal phenotype. In studies aimed at elucidating the physiol. basis for the SCR phenotype in class II mutants, the authors constructed full deletions of a number of them (inp52, yml128c, ylr219w, pet122), selecting for LEU2 and for drug-resistance substitutions. It was not possible to demonstrate reproducibly the SCR phenotype for any of these constructs. In addition, the SCR phenotype of LEU2 substitution mutants at the INP52, MSC1, MSC2, and MSC3 loci, newly constructed by the method described in the article, was variable in different isolates of the same confirmed genotype. Mutant isolates for all four loci manifested symptoms of mitotic chromosome instability. The observed increase in SCR frequency in some of the mutants and the dominant meiotic lethality that characterizes this class can be explained by aneuploidy resulting from chromosome instability. In Figure 1B, the phenotype designation (i.e., the + and - signs) under "Reductional" are transposed. In Table 1, the second DT84 should be DT85; DT90, omitted from the table, is DT71, except red1::TN+2166; DT154 is MATa/MATα; DT159, omitted from the table, is DT154, except rad24::TN+509; and DT111 should be DT71, except ypl108w::TN+25. The following information should be included in Table 1: DT170 is DT71 except yhr039c::TN+971.360.41 is DT167; 609 is DT166; 133 is DT165; 85 is DT64; 471 is DT107; 227 is DT161; 625 is DT168; 116-42 is DT69; and 1589 is DT171. On page 626, left column, the name of the plasmid carrying the dmc1::LEU2 allele should be changed from pNKY422 to pNKY459. In Table 2, class II mutants 360.41 and 471 were incorrectly footnoted h; the footnote should be f for "Transposon not in an identifiable structural gene.". The class III mutant yhr039c::TN+ 1583 should be changed to yhr039c::TN+ 971.

L41 ANSWER 2 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:499384 CAPLUS Full-text
DN 139:333779
TI Dissecting the pet18 mutation in Saccharomyces cerevisiae: HTL1 encodes a 7-kDa polypeptide that interacts with components of the RSC complex
AU Lu, Y.-M.; Lin, Y.-R.; Tsai, A.; Hsao, Y.-S.; Li, C.-C.; Cheng, M. Y.
CS School of Life Sciences, Institute of Genetics, National Yang-Ming University, Taichung, Taipei, 112, Taiwan
SO Molecular Genetics and Genomics (2003), 269(3), 321-330
CODEN: MGGOAA; ISSN: 1617-4615
PB Springer-Verlag
DT Journal
LA English
AB The yeast pet18 mutant exhibits three distinct phenotypes: temperature-sensitive lethality, failure to maintain a dsRNA virus, and respiration deficiency. We have isolated a yeast mutant, H53, with phenotypes identical to those of pet18. Based on PCR and Southern hybridization anal., H53 was found to result from a large chromosomal deletion extending from YCR019w to YCR028c on chromosome III. Genetic anal. was carried out on H53 to correlate individual loci with each of the observed phenotypes. Disruption of YCR020c-a/MAK31 brought about a loss of dsRNA without affecting the temperature sensitive phenotype. The loss of YCR020w-b/HTL1, which encodes a hypothetical protein of 78 amino acids in length, was shown to be responsible for the temperature-sensitive lethality of the H53 mutant. Using immunoblotting, we demonstrated that a 7-kDa protein was indeed expressed in wild-type yeast, but not in a HTL1 deletion mutant. Moreover, the significance of HTL1 was investigated by isolating genes that are functionally associated with HTL1. We demonstrated that Rsc8p interacts phys. with Htl1p, and that the genes RSC3, STH1 and RSC30 interact with HTL1. Thus, HTL1 may play a role in the function of the RSC complex.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 3 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2003:226353 CAPLUS Full-text
DN 139:1832
TI A General Strategy to Uncover Transcription Factor Properties Identifies a New Regulator of Drug Resistance in Yeast
AU Hikkel, Imrich; Lucau-Danila, Ancuta; Delaveau, Thierry; Marc, Philippe; Devaux, Frederic; Jacq, Claude
CS Laboratoire de Genetique Moleculaire, CNRS UMR8541, Ecole Normale Superieure, Paris, 75230, Fr.
SO Journal of Biological Chemistry (2003), 278(13), 11427-11432
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The authors demonstrate a genomewide approach to determine the physiol. role of a putative transcription factor, Ylr266, identified through yeast genome sequencing program. The authors constructed activated forms of the zinc finger (Zn2Cys6) protein Ylr266, and the authors analyzed the corresponding transcriptomes with DNA microarrays to characterize the up-regulated genes. The direct target genes of Ylr266 were further identified by in vivo chromatin immunopptn. procedure. The functions of the genes directly controlled by YLR266c are in agreement with the observed drug-resistance phenotype of the cell expressing an activated form of Ylr266. These target genes code for ATP-binding cassette or major facilitator superfamily transporters such as PDR15, YOR1, or AZR1 or for other proteins such as SNG1, YJL216c, or YLL056c which are already known to be involved in the yeast pleiotropic drug resistance (PDR) phenomenon. YLR266c could thus be named PDR8. Overlaps with the other PDR networks argue in favor of a new specific role for PDR8 in connection with the well known PDR regulators PDR1/PDR3 and YRR1. This strategy to identify the regulatory properties of an anonymous transcription factor is likely to be generalized to all the Zn2Cys6 transcription factors from Saccharomyces cerevisiae and related yeasts.
OSC.G 31 THERE ARE 31 CAPLUS RECORDS THAT CITE THIS RECORD (31 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 4 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:575185 CAPLUS Full-text
DN 137:136702
TI Protein-protein interactions in Saccharomyces cerevisiae and the identification of selected interacting domains using two hybrid screening
IN Legrain, Pierre
PA Hybrigenics, Fr.
SO PCT Int. Appl., 196 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002059255	A2	20020801	WO 2002-EP1350	20020125
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2002231791	A1	20020806	AU 2002-231791	20020125
PRAI US 2001-264577P	P	20010126		
WO 2002-EP1350	W	20020125		

AB The present invention relates to proteins that interact with other proteins of Saccharomyces cerevisiae. More specifically, the present invention relates to complexes of polypeptides or polynucleotides encoding the polypeptides, fragments of the polypeptides, antibodies to the complexes, Selected Interacting Domains (SID) which are identified due to the protein-protein interactions, methods for screening for agents which modulate the interaction of proteins and compns. that are capable of modulating the protein-protein interactions, such as, for example, drug in pharmaceutical composition

L41 ANSWER 5 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:479051 CAPLUS Full-text
DN 137:197396
TI SDT1/SSM1, a multicopy suppressor of S-II null mutant, encodes a novel pyrimidine 5'-nucleotidase
AU Nakanishi, Toshiyuki; Sekimizu, Kazuhisa
CS Discovery Research Laboratories, Daiichi Pharmaceutical Company, Ltd., Tokyo, 134-8630, Japan
SO Journal of Biological Chemistry (2002), 277(24), 22103-22106
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB SDT1 (suppressor of disruption of TFIIS 1, YGL224c, also known as SSM1, suppressor of S-II null mutant 1) is a Saccharomyces cerevisiae gene identified as a multicopy suppressor of 6-azauracil sensitivity in a null mutant of the transcription elongation factor S-II. We found that overprodn. of SDT1 caused hyposensitivity to not only 6-azauracil but also 5-fluorouracil and 5-fluorocytosine. This hyposensitivity was limited to pyrimidine derivs., and no effect was observed for non-pyrimidine drugs including such clin. used anti-fungal drugs as amphotericin B and fluconazole. Purified recombinant SDT1 protein specifically dephosphorylated 5'-UMP and 5'-CMP. These results suggested that SDT1 conferred pyrimidine-specific hyposensitivity by dephosphorylating active metabolites of 6- or 5-modified pyrimidines, i.e. 6- or 5-modified UMP. This is the first description of a highly specific pyrimidine 5'-nucleotidase in S. cerevisiae.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 6 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:385644 CAPLUS Full-text
DN 137:106352
TI Large-scale identification of genes important for apical growth in Saccharomyces cerevisiae by directed allele replacement technology (DART) screening
AU Bidlingmaier, Scott; Snyder, Michael
CS Department of Molecular, Cellular and Developmental Biology, Yale University, New Haven, CT, 06520-8103, USA
SO Functional & Integrative Genomics (2002), 1(6), 345-356
CODEN: FIGUBY; ISSN: 1438-793X
PB Springer-Verlag
DT Journal
LA English
AB In S. cerevisiae, apical bud growth occurs for a brief period in G1 when the deposition of membrane and cell wall is restricted to the tip of the growing bud. To identify genes important for apical bud growth, we have utilized a novel transposon-based mutagenesis system termed DART (Directed Allele Replacement Technol.) that allows the rapid transfer of defined insertion alleles into any strain background. A total of 4,810 insertion alleles affecting 1,392 different yeast genes were transferred into a cdc34-2 mutant strain that arrests in the apical growth phase when grown at the restrictive temperature of 37°. We identified 29 insertion alleles, containing mutations in 17 different genes (SMY1, SPA2, PAN1, SLA1, SLA2, CBK1, SEC22, FAB1, VPS36, VID22, RAS2, ECM33, OPI3, API1/YDR372c, API2/YDR525w, API3/YKR020w, and API4/YNL051w), which alter the elongated bud morphol. of cdc34-2 cells arrested in the apical growth phase. Upon treatment with mating pheromone at 25°, cells containing insertion alleles affecting 10 of these genes (SMY1, SPA2, PAN1, SLA1, SLA2, CBK1, FAB1, VPS36, VID22, and API2/YDR525w) form abnormal mating projections. Addnl., cells containing insertion alleles affecting SEC22, RAS2, API1/YDR372c, API3/YKR020w, and API4/YNL051 display severe mating projection formation defects at the elevated temperature of 37°. DART mutagenesis has many advantages over traditional mutagenesis methods and will be a useful tool for dissecting gene networks important for biol. processes.
OSC.G 26 THERE ARE 26 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 7 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2002:86332 CAPLUS Full-text
DN 137:28901
TI Ctf3p, the Mis6 budding yeast homolog, interacts with Mcm22p and Mcm16p at the yeast outer kinetochore
AU Measday, Vivien; Hailey, Dale W.; Pot, Isabelle; Givan, Scott A.; Hyland, Katherine M.; Cagney, Gerard; Fields, Stan; Davis, Trisha N.; Hieter, Philip
CS The Centre for Molecular Medicine and Therapeutics, Department of Medical Genetics, University of British Columbia, Vancouver, BC, V5Z 4H4, Can.
SO Genes & Development (2002), 16(1), 101-113
CODEN: GEDEEP; ISSN: 0890-9369
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB The budding yeast kinetochore is composed of an inner and outer protein complex, which binds to centromere (CEN) DNA and attaches to microtubules. We performed a genetic synthetic dosage lethality screen to identify novel kinetochore proteins in a collection of chromosome transmission fidelity mutants. Our screen identified several new kinetochore-related proteins including YLR381Wp/Ctf3p, which is a member of a conserved family of centromere-binding proteins. Ctf3p interacts with Mcm22p, Mcm16p, and the outer kinetochore protein Ctf19p. We used chromatin immunopptn. to demonstrate that Ctf3p, Mcm22p, and Mcm16p bind to CEN DNA in a Ctf19p-dependent manner. In addition, Ctf3p, Mcm22p, and Mcm16p have a localization pattern similar to other kinetochore proteins. The fission yeast Ctf3p homolog, Mis6, is required for loading of a CENP-A centromere specific histone, Cnp1, onto centromere DNA. We find however that Ctf3p is not required for loading of the budding yeast CENP-A homolog, Cse4p, onto CEN DNA. In contrast, Ctf3p and Ctf19p fail to bind properly to the centromere in a cse4-1 mutant strain. We conclude that the requirements for CENP-A loading onto centromere DNA differ in fission vs. budding yeast.
OSC.G 73 THERE ARE 73 CAPLUS RECORDS THAT CITE THIS RECORD (73 CITINGS)
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 8 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:915888 CAPLUS Full-text
DN 136:161918
TI Systematic genetic analysis with ordered arrays of yeast deletion mutants
AU Tong, Amy Hin Yan; Evangelista, Marie; Parsons, Ainslie B.; Xu, Hong; Bader, Gary D.; Page, Nicholas; Robinson, Mark; Raghibizadeh, Sasan; Hogue, Christopher W. V.; Bussey, Howard; Andrews, Brenda; Tyers, Mike; Boone, Charles
CS Banting and Best Department of Medical Research, University of Toronto, Toronto, ON, M5G 1LG, Can.
SO Science (Washington, DC, United States) (2001), 294(5550), 2364-2368
CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English
AB In Saccharomyces cerevisiae, more than 80% of the .apprx.6200 predicted genes are nonessential, implying that the genome is buffered from the phenotypic consequences of genetic perturbation. To evaluate function, we developed a method for systematic construction of double mutants, termed synthetic genetic array (SGA) anal., in which a query mutation is crossed to an array of .apprx.4700 deletion mutants. Inviable double-mutant meiotic progeny identify functional relationships between genes. SGA anal. of genes with roles in cytoskeletal organization (BNI1, ARP2, ARC40, BIM1), DNA synthesis and repair (SGS1, RAD27), or uncharacterized functions (BBC1, NBP2) generated a network of 291 interactions among 204 genes. Systematic application of this approach should produce a global map of gene function.
OSC.G 847 THERE ARE 847 CAPLUS RECORDS THAT CITE THIS RECORD (851 CITINGS)
RE.CNT 34 THERE ARE 34 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 9 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:892884 CAPLUS Full-text
DN 136:364531
TI Genes required for ionizing radiation resistance in yeast
AU Bennett, Craig B.; Lewis, L. Kevin; Karthikeyan, Gopalakrishnan; Lobachev, Kirill S.; Jin, Yong H.; Sterling, Joan F.; Snipe, Joyce R.; Resnick, Michael A.
CS Laboratory of Molecular Genetics, National Institute of Environmental Health Sciences, Research Triangle Park, NC, 27709, USA
SO Nature Genetics (2001), 29(4), 426-434
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America Inc.
DT Journal
LA English
AB The ability of Saccharomyces cerevisiae to tolerate ionizing radiation damage requires many DNA-repair and checkpoint genes, most having human orthologs. A genome-wide screen of diploid mutants homozygous with respect to deletions of 3,670 nonessential genes revealed 107 new loci that influence γ-ray sensitivity. Many affect replication, recombination and checkpoint functions. Nearly 90% were sensitive to other agents, and most new genes could be assigned to the following functional groups: chromatin remodeling, chromosome segregation, nuclear pore formation, transcription, Golgi/vacuolar activities, ubiquitin-mediated protein degradation, cytokinesis, mitochondrial activity and cell wall maintenance. Over 50% share homol. with human genes, including 17 implicated in cancer, indicating that a large set of newly identified human genes may have related roles in the toleration of radiation damage.
OSC.G 180 THERE ARE 180 CAPLUS RECORDS THAT CITE THIS RECORD (180 CITINGS)
RE.CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 10 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2001:543499 CAPLUS Full-text
DN 136:178678
TI Functional analysis of six ORFs from Saccharomyces cerevisiae chromosome IV: two-spored asci produced by disruptant of YDR027c and strain-dependent DNA heterogeneity around YDR036c
AU Aittamaa, Marja; Turakainen, Hilkka; Korhola, Matti
CS Division of General Microbiology, Department of Biosciences, FIN-00014, Finland
SO Yeast (2001), 18(10), 931-941
CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Six S. cerevisiae FY1679 heterozygous deletion mutants were made by replacing six open reading frames (ORFs) of the chromosome IV right arm with kanMX4 selection marker. Haploid and homozygous diploid deletion mutants were obtained from sporulation, dissection and mating expts. No essential genes were found. The basic phenotypic anal. showed that the haploid and homozygous deletants for the ORF YDR027c (LUV1, VSP54 or RK11) grew slowly. The diploid homozygous deletants for this ORF had a low frequency of sporulation. They produced asci with no more than one or two haploid spores and the majority of these spores formed were not viable. The deletion of the other ORFs, YDR022c (CIS1), YDR030c (RAD28), YDR032c (PST2), YDR033w (MRH1) and YDR036c, did not change the phenotypes tested in strain FY1679 or the first four ORFs in strain CEN.PK2. This work showed some differences in the DNA sequences between FY1679 and CEN.PK2: the regions immediately 1 kb upstream from YDR036c in these two strains are too different to hybridize properly, preventing deletion of YDR036c in the CEN.PK2 background by recombination with a disruption cassette designed for FY1679. In addition, there are different sets of transposable elements on the other side of the ORF, the differences starting at about 3.5 kb downstream from YDR036c.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 11 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:735504 CAPLUS Full-text
DN 134:261728
TI Prediction of protein interactions: metabolic enzymes are frequently involved in gene fusion
AU Tsoka, Sophia; Ouzounis, Christos A.
CS Computational Genomics Group, Research Programme, The European Bioinformatics Institute, EMBL Cambridge Outstation, Cambridge, UK
SO Nature Genetics (2000), 26(2), 141-142
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America Inc.
DT Journal
LA English
AB The genomes of 15 species were fount to contain fused proteins homologous to Escherichia coli enzymes showing that known metabolic enzymes exhibit a threefold preference for gene fusions compared to controls. One of six metabolic enzymes of E. coli appears to participate in a fusion event. Complex formation of multimeric enzymes, multiple fusions or paralogy, and species distribution of the composite proteins were traced. There was a high percentage of subunits of enzyme complexes involved in gene fusions. Redundancy of component proteins increases the number of detected fusions, e.g., AroK and AroE both detected AroD as a likely partner, with both pairs mapping to the penta-functional aromatic biosynthesis enzyme YDR127w from yeast. The four species with the highest number of composite proteins were Saccharomyces cerevisiae, Bacillus subtilis, Caenorhabditis elegans, and Mycobacterium tuberculosis. Only 4.4% of random proteins seem to be involved in gene fusion.
OSC.G 54 THERE ARE 54 CAPLUS RECORDS THAT CITE THIS RECORD (54 CITINGS)
RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 12 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:707339 CAPLUS Full-text
DN 133:277150
TI Methods for identifying pathway-specific genes and their uses for drug screening or as drug targets
IN Roberts, Christopher J.
PA Rosetta Inpharmatics, Inc., USA
SO PCT Int. Appl., 239 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000058520	A1	20001005	WO 2000-US8555	20000329
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 20030211475	A1	20031113	US 2001-946290	20010905
PRAI US 1999-282243	A	19990331		

AB The present invention relates to methods for identifying one or more reporter genes for a particular biol. pathway of interest. The reporter genes of this invention are particularly useful for analyzing the activity of particular biol. pathways of interest, and may be further used in the design of drugs, drug therapies or other biol. agents (e.g., insecticides, herbicides, fungicides, antibiotics, or antivirals) to target a particular biol. pathway. The present invention also relates to methods for identifying one or more target genes for a particular biol. pathway of interest. Target genes of the invention are useful as specific targets for drugs which may be designed to enhance, inhibit, or modulate a particular biol. pathway. Methods to identify genes which modify the function or structure of a member (e.g., compound or gene product) of a particular biol. pathway are provided. Thus, DNA arrays were used to identify Saccharomyces cerevisiae genes involved in ergosterol biosynthesis, in the protein kinase C pathway, or in the "invasive growth" pathway.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 13 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:324538 CAPLUS Full-text
DN 133:146522
TI Saccharomyces cerevisiae RAI1 (YGL246c) is homologous to human DOM3Z and encodes a protein that binds the nuclear exoribonuclease Rat1p
AU Xue, Yang; Bai, Xinxue; Lee, Insuk; Kallstrom, George; Ho, Jennifer; Brown, Justin; Stevens, Audrey; Johnson, Arlen W.
CS Section of Molecular Genetics and Microbiology and Institute for Cellular and Molecular Biology, University of Texas at Austin, Austin, TX, 78712-1095, USA
SO Molecular and Cellular Biology (2000), 20(11), 4006-4015
CODEN: MCEBD4; ISSN: 0270-7306
PB American Society for Microbiology
DT Journal
LA English
AB The RAT1 gene of Saccharomyces cerevisiae encodes a 5' → 3' exoribonuclease which plays an essential role in yeast RNA degradation and/or processing in the nucleus. We have cloned a previously uncharacterized gene (YGL246c) that we refer to as RAI1 (Rat1p interacting protein 1). RAI1 is homologous to Caenorhabditis elegans DOM-3 and human DOM3Z. Deletion of RAI1 confers a growth defect, which can be complemented by an addnl. copy of RAT1 on a centromeric vector or by directing Xrn1p, the cytoplasmic homolog of Rat1p, to the nucleus through the addition of a nuclear targeting sequence. Deletion of RAI1 is synthetically lethal with the rat1-1ts mutation and shows genetic interaction with a deletion of SKI2 but not XRN1. Polysome anal. of a RAI1 deletion mutant indicated a defect in 60S biogenesis which was nearly fully reversed by high-copy RAT1. Northern blot anal. of rRNAs revealed that RAI1 is required for normal 5.8S processing. In the absence of RAI1, 5.8SL was the predominant form of 5.8S, and there was an accumulation of 3'-extended forms but not 5'-extended species of 5.8S. In addition, a 27S pre-rRNA species accumulated in the RAI1 mutant. Thus, deletion of RAI1 affects both 5' and 3' processing reactions of 5.8S rRNA. Consistent with the in vivo data suggesting that RAI1 enhances RAT1 function, purified Rai1p stabilized the in vitro exoribonuclease activity of Rat1p.
OSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 14 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 2000:276930 CAPLUS Full-text
DN 133:28351
TI The f-box protein Rcy1p is involved in endocytic membrane traffic and recycling out of an early endosome in Saccharomyces cerevisiae
AU Wiederkehr, Andreas; Avaro, Sandrine; Prescianotto-Baschong, Cristina; Haguenauer-Tsapis, Rosine; Riezman, Howard
CS Biozentrum of the University of Basel, Basel, CH-4056, Switz.
SO Journal of Cell Biology (2000), 149(2), 397-410
CODEN: JCLBA3; ISSN: 0021-9525
PB Rockefeller University Press
DT Journal
LA English
AB In S. cerevisiae, endocytic material is transported through different membrane-bound compartments before it reaches the vacuole. In a screen for mutants that affect membrane trafficking along the endocytic pathway, a novel mutant disrupted for the gene YJL204c was identified that was renamed RCY1 (recycling 1). Deletion of RCY1 leads to an early block in the endocytic pathway before the intersection with the vacuolar protein sorting pathway. Mutation of RCY1 leads to the accumulation of an enlarged compartment that contains the t-SNARE Tlg1p and lies close to areas of cell expansion. In addition, endocytic markers such as Ste2p and the fluorescent dyes Lucifer yellow and FM4-64 were found in a similar enlarged compartment after their internalization. To determine whether rcy1Δ is defective for recycling, an assay that measures the recycling of previously internalized FM4-64 was developed. This method allows following the recycling pathway in yeast in real time. Using this assay, it could be demonstrated that recycling of membranes is rapid in S. cerevisiae and that a major fraction of internalized FM4-64 is secreted back into the medium within a few minutes. The rcy1Δ mutant is strongly defective in recycling.
OSC.G 89 THERE ARE 89 CAPLUS RECORDS THAT CITE THIS RECORD (89 CITINGS)
RE.CNT 63 THERE ARE 63 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 15 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:514248 CAPLUS Full-text
DN 131:269376
TI Chemotyping of yeast mutants using robotics
AU Rieger, Klaus-Jorg; El-Alama, Mohamed; Stein, Georg; Bradshaw, Charles; Slonimski, Piotr P.; Maundrell, Kinsey
CS Centre de Genetique Moleculaire du Centre National de la Recherche Scientifique, Laboratoire Propre Associe a L'Universite Pierre et Marie Curie, Gif-sur-Yvette, F-91198, Fr.
SO Yeast (1999), 15(10B), 973-986
CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB By now, the EUROFAN program for the functional anal. of genes from the yeast genome has attained its cruising speed. Indeed, several hundreds of yeast mutants with no phenotype as tested by growth on standard media and no significant sequence similarity to proteins of known function are available through the efforts of various labs. Based on the methodol. initiated during the pilot project on yeast chromosome III (Yeast 13, 1547-1562, 1997) we adapted it to High Throughput Screening (HTS), using robotics. The first 100 different gene deletions from EUROSCARF, constructed in an FY1679 strain background, were run against a collection of about 300 inhibitors. Many of these inhibitors have not been reported until now to interfere in vivo with growth of Saccharomyces cerevisiae. In the present paper we provide a list of novel growth conditions and a compilation of 49 yeast deletants (from chromosomes II, IV, VII, X, XIV, XV) corresponding to 58% of the analyzed genes, with at least one clear and stringent phenotype. The majority of these deletants are sensitive to one or two compds. (monotropic phenotype) while a distinct subclass of deletants displays a hyper-pleiotropic phenotype with sensitivities to a dozen or more compds. Therefore, chemotyping of unknown genes with a large spectrum of drugs opens new vistas for a more in-depth functional anal. and a more precise definition of mol. targets.
OSC.G 42 THERE ARE 42 CAPLUS RECORDS THAT CITE THIS RECORD (42 CITINGS)
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 16 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:514246 CAPLUS Full-text
DN 131:267781
TI Construction and genetic analysis of S. cerevisiae deletants of six novel ORFs from chromosome II
AU Malagon, Francisco; Aguilera, Andres
CS Departamento de Genetica, Facultad de Biologia, Universidad de Sevilla, Seville, 41012, Spain
SO Yeast (1999), 15(10B), 955-961
CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB We have constructed S. cerevisiae strains carrying genomic deletions of six ORFs from the left arm of chromosome II (YBL018c, YBL019w, YBL024w, YBL042c, YBL043w and YBL046w) in both FY1679 and W303 backgrounds. We have found that YBL018c is an essential gene in yeast, whereas the other five genes are non-essential. We have developed plasmids carrying deletion cassettes that can be used to delete any of the six genes in S. cerevisiae by transforming to G418-resistance, as well as centromeric plasmids containing the cognate genes.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 17 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:449831 CAPLUS Full-text
DN 131:224200
TI Deletion of 24 open reading frames from chromosome XI from Saccharomyces cerevisiae and phenotypic analysis of the deletants
AU Zuniga, Sonia; Boskovic, Jasminka; Garcia-Cantalejo, Jesus M.; Jimenez, Antonio; Ballesta, Juan P. G.; Remacha, Miguel
CS CSIC and Centro de Biologia Molecular 'Severo Ochoa', UAM, Madrid, 28049, Spain
SO Gene (1999), 233(1-2), 141-150
CODEN: GENED6; ISSN: 0378-1119
PB Elsevier Science B.V.
DT Journal
LA English
AB As a part of the EUROFAN program, 24 open reading frames from Saccharomyces cerevisiae (YKR010c to YKR013w, YKR015c to YKR025w, YKR081c to YKR083c, YKR087c to YKR091w and YKR096w) were disrupted in two genetic backgrounds, FY1679 and W303. Systematic deletions and phenotypic anal. were performed following a hierarchical strategy, the so-called 'mass murder'. Of the 24 genes thus deleted, four are essential, whereas the deletion of 17 did not reveal any significant difference between the parental and mutant strains. Deletions of the remaining three show some growth phenotype; ykr024c mutants grow slowly under any conditions, ykr019c mutants grow slower in a rich medium and ykr082w mutants are temperature sensitive, being unable to germinate at 30°C and above.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 18 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:135065 CAPLUS Full-text
DN 130:348007
TI Disruption and basic phenotypic analysis of 18 novel genes from the yeast Saccharomyces cerevisiae
AU Wysocki, Robert; Roganti, Tiziana; Van Dyck, Eric; De Kerchove D'Exaerde, Alban; Foury, Francoise
CS Unite de Biochimie Physiologique, Universite Catholique de Louvain, Louvain-la-Neuve, B-1348, Belg.
SO Yeast (1999), 15(2), 165-171
CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB In the frame of the European Network for Functional Anal. (EUROFAN) we have deleted 18 yeast open reading frames (ORFs) from chromosomes II, X and XIV using the short flanking homol.-PCR strategy. Two diploid strains were used: FY1679 and CEN.PK2. The deletion kanMX6 cassettes with long flanking homol. and the cognate gene clones have also been constructed. Heterozygous diploid deletant strains have been sporulated. Tetrad anal. revealed that all the ORFs studied were non-essential. However, four deletant strains exhibited phenotypes. The YBL025wΔ strain showed extremely slow cellular growth under all conditions tested. The YJL204cΔ strain grew slower than wild-type at 30° and 37°, was cold-sensitive, and the homozygous diploids did not sporulate. The YNL213cΔ strain did not grow on glycerol and had lost mitochondrial DNA. The deletion of YNL215w caused slower growth on all media but the defect was more pronounced on glucose-minimal and glycerol-rich media than on glucose-rich medium. All deletion mutants were complemented by the corresponding plasmid borne cognate gene. The YJL204w, YNL213c and YNL215w ORFs do not bear significant homol. to proteins of known function. YBL025w has recently been identified as RRN10, a gene that encodes an RNA polymerase I-specific transcription initiator factor. The deletion of the remaining fourteen ORFs did not reveal any mutant phenotype in our basic growth tests.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 19 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1999:52 CAPLUS Full-text
DN 130:150308
TI Molecular characterization of Saccharomyces cerevisiae Δ3,Δ2-enoyl-CoA isomerase
AU Geisbrecht, Brian V.; Zhu, Dai; Schulz, Kerstin; Nau, Katja; Morrell, James C.; Geraghty, Michael; Schulz, Horst; Erdmann, Ralf; Gould, Stephen J.
CS Departments of Biological Chemistry and Pediatrics, The Johns Hopkins University School of Medicine, Baltimore, MD, 21205, USA
SO Journal of Biological Chemistry (1998), 273(50), 33184-33191
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The authors report the identification of the Saccharomyces cerevisiae peroxisomal Δ3,Δ2-enoyl-CoA isomerase, and enzyme that is essential for the β-oxidation of unsatd. fatty acids. The yeast gene YLR284C was identified in an in silico screen or genes that contain an oleate response element, a transcription factor-binding site common to most fatty acid-induced genes. Growth on oleic acid resulted in a significant increase in YLR284C mRNA, demonstrating that it is indeed an oleate-induced gene. The deduced product of YLR284C contains a type 1 peroxisomal targeting signal-like sequence at its C terminus and localizes to the peroxisome in a PEX8-dependent manner. Removal of YLR284C from the S. cerevisiae genome eliminated growth on oleic acid, but had no effect on peroxisome biogenesis, indicating a role for YLR284C in fatty acid metabolism Cells lacking YLR284C had no detectable Δ3,Δ2-enoyl-CoA isomerase activity, and a bacterially expressed form of this protein catalyzed the isomerization of 3-cis-octenoyl-CoA to 2-trans-octenoyl-CoA with a specific activity of 16 units/mg. The authors conclude that YLR284C encodes the yeast peroxisomal Δ3,Δ2-enoyl-CoA isomerase and propose a new name, ECI1, to reflect its enoyl-CoA isomerase activity.
OSC.G 46 THERE ARE 46 CAPLUS RECORDS THAT CITE THIS RECORD (46 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 20 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:746289 CAPLUS Full-text
DN 130:108109
TI When overexpressed, a novel centrosomal protein, RanBPM, causes ectopic microtubule nucleation similar to γ-tubulin
AU Nakamura, Masafumi; Masuda, Hirohisa; Horii, Johji; Kuma, Kei-Ichi; Yokoyama, Nobuhiko; Ohba, Tomoyuki; Nishitani, Hideo; Miyata, Takashi; Tanaka, Masao; Nishimoto, Takeharu
CS Department of Molecular Biology, Graduate School of Medical Science, Kyushu University, Fukuoka, 812-82, Japan
SO Journal of Cell Biology (1998), 143(4), 1041-1052
CODEN: JCLBA3; ISSN: 0021-9525
PB Rockefeller University Press
DT Journal
LA English
AB A novel human protein with a mol. mass of 55 kDa, designated RanBPM, was isolated with the two-hybrid method using Ran as a bait. Mouse and hamster RanBPM possessed a polypeptide identical to the human one. Furthermore, Saccharomyces cerevisiae was found to have a gene, YGL227w, the C-terminal half of which is 30% identical to RanBPM. Anti-RanBPM antibodies revealed that RanBPM was localized within the centrosome throughout the cell cycle. Overexpression of RanBPM produced multiple spots which were colocalized with γ-tubulin and acted as ectopic microtubule nucleation sites, resulting in a reorganization of microtubule network. RanBPM cosedimented with the centrosomal fractions by sucrose-d. gradient centrifugation. The formation of microtubule asters was inhibited not only by anti-RanBPM antibodies, but also by nonhydrolyzable GTP-Ran. Indeed, RanBPM specifically interacted with GTP-Ran in two-hybrid assay. The central part of asters stained by anti-RanBPM antibodies or by the mAb to γ-tubulin was faded by the addition of GTPγS-Ran, but not by the addition of anti-RanBPM antibodies. These results provide evidence that the Ran-binding protein, RanBPM, is involved in microtubule nucleation, thereby suggesting that Ran regulates the centrosome through RanBPM.
OSC.G 123 THERE ARE 123 CAPLUS RECORDS THAT CITE THIS RECORD (123 CITINGS)
RE.CNT 88 THERE ARE 88 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 21 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:704618 CAPLUS Full-text
DN 130:63409
TI Interaction of Bnr1p with a novel Src homology 3 domain-containing Hof1p. Implication in cytokinesis in Saccharomyces cerevisiae
AU Kamei, Takashi; Tanaka, Kazuma; Hihara, Taro; Umikawa, Masato; Imamura, Hiroshi; Kikyo, Mitsuhiro; Ozaki, Kumi; Takai, Yoshimi
CS Department of Molecular Biology and Biochemistry, Osaka University Medical School, Suita, 565-0871, Japan
SO Journal of Biological Chemistry (1998), 273(43), 28341-28345
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Proteins containing the formin homol. (FH) domains FH1 and FH2 are involved in cytokinesis or establishment of cell polarity in a variety of organisms. We have shown that the FH proteins Bni1p and Bnr1p are potential targets of the Rho family small GTP-binding proteins and bind to an actin-binding protein, profilin, at their proline-rich FH1 domains to regulate reorganization of the actin cytoskeleton in the yeast Saccharomyces cerevisiae. We found here that a novel Src homol. 3 (SH3) domain-containing protein, encoded by YMR032w, interacted with Bnr1p in a GRP-Rho4p-dependent manner through the FH1 domain of Bnr1p and the SH3 domain of Ymr032wp. Ymr032wp weakly bound to Bni1p. Ymr032wp was homologous to cdc15p, which is involved in cytokinesis in Schizosaccharomyces pombe, and we named this gene HOF1 (homolog of cdc 15). Both Bnr1p and Hof1p were localized at the bud neck, and both the bnr1 and hof1 mutations showed synthetic lethal interactions with the bni1 mutation. The hof1 mutant cells showed phenotypes similar to those of the septin mutants, indicating that HOF1 is involved in cytokinesis. These results indicate that Bnr1p directly interacts with Hof1p as well as with profilin to regulate cytoskeletal functions in S. cerevisiae.
OSC.G 92 THERE ARE 92 CAPLUS RECORDS THAT CITE THIS RECORD (92 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 22 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:559535 CAPLUS Full-text
DN 129:255837
OREF 129:51995a,51998a
TI The uracil permease of Schizosaccharomyces pombe: a representative of a family of 10 transmembrane helix transporter proteins of yeasts
AU De Montigny, J.; Straub, M. L.; Wagner, R.; Bach, M. L.; Chevallier, M. R.
CS Lab. Microbiologie Genetique, UPRES A-7010-CNRS, Institut de Botanique, Univ. Louis Pasteur Strasbourg, Strasbourg, F-67083, Fr.
SO Yeast (1998), 14(11), 1051-1059
CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The uracil permease gene of Schizosaccharomyces pombe was cloned and sequenced. The deduced protein sequence shares strong similarities with five open reading frames from Saccharomyces cerevisiae, namely the uracil permease encodeed by the FUR4 gene, the allantoin permease encoded by DAL4, a putative uridine permease (YBL042C) and two unknown ORFs YOR071c and YLR237w.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 23 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1998:299370 CAPLUS Full-text
DN 129:37099
OREF 129:7701a,7704a
TI A 9359 bp fragment from the right arm of Saccharomyces cerevisiae chromosome VII includes the FOL2 and YTA7 genes and three unknown open reading frames
AU Carbone, M. L. Agostoni; Lucchini, G.; Melchioretto, P.; Nardese, V.; Vanoni, M.; Panzeri, L.
CS Dipartimenti di Genetica e di Biologia dei Microrganismi, Universita di Milano, Milan, 20133, Italy
SO Yeast (1998), 14(6), 587-591
CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB In the framework of the EU program for systematic sequencing of the Saccharomyces cerevisiae genome we determined the sequence of a 9359 bp fragment of the right arm of chromosome VII. Five open reading frames (ORFs) of at least 300 nucleotides were found in this region. YGR267c encodes a protein with significant similarity to the enzyme GTP-cyclohydrolase I, that controls the first step in the biosynthetic pathway leading to various pterins and shows a high degree of sequence conservation from bacteria to mammals. We have recently demonstrated that YGR267c corresponds to the FOL2 gene, previously localized in the same chromosomal region by genetic mapping. The protein deduced from YGR270w belongs to the superfamily of putative ATPases associated with diverse cellular activities. It corresponds to the YTA7 gene, a member of a set of yeast genes coding for putative ATPases with high similarity to constituents of the 26S protease. The three ORFs YGR266w, YGR268c and YGR269w encode putative products of unknown function, with neither significant similarity to proteins in databases nor recognizable domains. YGR268c and YGR269w are partially overlapping ORFs: YGR268c seems to correspond to a real gene, whereas YGR269w is probably a fortuitous ORF. The sequence has been entered in the EMBL data library under Accession Number Y07893.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L41 ANSWER 24 OF 24 CAPLUS COPYRIGHT 2011 ACS on STN
AN 1997:764256 CAPLUS Full-text
DN 128:163520
OREF 128:32095a,32098a
TI Two genes of the putative mitochondrial fatty acid synthase in the genome of Saccharomyces cerevisiae
AU Schneider, R.; Brors, Benedikt; Burger, Frank; Camrath, Stefan; Weiss, Hanns
CS Institut fur Biochemie, Heinrich-Heine-Universitat Dusseldorf, Universitatsstrasse 1, Dusseldorf, 40225, Germany
SO Current Genetics (1997), 32(6), 384-388
CODEN: CUGED5; ISSN: 0172-8083
PB Springer-Verlag
DT Journal
LA English
AB In order to find further genes of the mitochondrial fatty acid synthase, the genome of Saccharomyces cerevisiae was searched for sequences that are homologous to conserved regions of bacterial fatty acid synthase genes. The gene products of ORF YKL055c (EMBL Accession Number X75781) and of YOR221C (EMBL Accession No.X92441) were found to be homologous to bacterial 3-oxoacyl-(acyl carrier protein) reductases and to malonyl-CoA:ACP-transferases, resp. These two genes were disrupted which in both cases led to a respiratory deficient phenotype, as is the case for the genes encoding a mitochondrial acyl carrier protein and a β-ketoacyl-ACP synthase. It is proposed that the above mentioned genes be called OAR1 [3-oxo-acyl-(acyl carrier protein) reductase] and MCT1 (malonyl-CoA:ACP transferase). They are presumed to be part of a type-II mitochondrial fatty acid synthase, a relic of the endosymbiontic origin of mitochondria, delivering substrates for phospholipid re-modeling and/or repair.
OSC.G 47 THERE ARE 47 CAPLUS RECORDS THAT CITE THIS RECORD (47 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

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(FILE 'HOME' ENTERED AT 16:32:16 ON 25 SEP 2011)

FILE 'CAPLUS' ENTERED AT 16:34:05 ON 25 SEP 2011
L1 522 S (YKL?)/BI,AB
L2 9 S (YBL056W OR YDR149C OR YLR285W OR YLR311C)/BI,AB
L3 14 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C ORYGL24
L4 9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L5 4 S (YLR312C OR YLR315C OR YLR320W OT YPL030W)/BI,AB
L6 6 S (YKL080W OR YLR447C OR YHR06W OR YPR036W OR YHR039C? OR YHR02
L7 12 S (YGL026C OR YGR180C OR YDR127W OR YCR028C OR YLR284C OR YOR22
L8 10 S (YBL042C OR YDR148C OR YHL025W OR YLR307W OR YLR345W OR YLR35
L9 12 S (YGR180C OR YDR150W OR YGL240W OT YBL058W OR YIL036W OR YLR22
L10 6 S (YPL018W OR YBL063W OR YDR363W? OR YIR026C OR YLR234W OR YMR0
L11 7 S (YGR006W OR YIL036W OR YKR082W OR YLR226W OR YML112W OR YMR02
L12 7 S (YBR279W OR YGL070C OR YGL071W OR YGL222C OR YHL025W OR YLR26
L13 4 S (YBL058W OR YLR287C? OR YGR0844C OR YLR344W)/BI,AB
L14 3 S (YKL080W OR YLR447C OR YGL240W OR YGR105W OR YGL206C)/BI,AB
L15 6 S (YKL119C OR YDR414C OR YHR060W OR YLR292C OR YLR306W OR YGL22
L16 10 S (YPR036W OR YDR027C OR YHR039C OR YKL080W OR YLR447C OR YGL20
L17 3 S (YJR104C OR YMR021C)/BI,AB
L18 5 S (YPR036W OR YHR039C? OR YKL080W OR YLR447C OR YGL071W OR YIR0
L19 4 S (YDL151C OR YBL058W)/BI,AB
L20 8 S (YKR082W OR YDL151C OR YOL068C OR YDR363W? OR YHL025W OR YIR0
L21 5 S (YDR027C OR YDR414C OR YLR381W ORYGR084C OR YMR032W)/BI,AB
L22 8 S (YPR036W OR YHR026W OR YHR039C OR YKL080W OR YLR447C OR YCR02
L23 2 S YBL056W/BI,AB
L24 9 S (YDR149C OR YLR285W OR YLR311C)/BI,AB
L25 16 S (YOR331C OR YPR123C OR YDR525W? OR YDR539W OR YDR540C OR YGL2
L26 9 S (YLR282C OR YLR287C OR YLR290C OR YJL188C OR YJL192C OR YJL21
L27 7 S (YLR312C OR YLR315W OR YLR320W OR YPL030W)/BI,AB

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L28          25 S L2 OR L3 OR L4 OR L5
L29          27 S L6 OR L7 OR L8 OR L9 OR L10
L30          13 S L11 OR L12 OR L13 OR L14 OR L15
L31          13 S L16 OR L17 OR L18 OR L19 OR L20
L32          34 S L21 OR L22 OR L23 OR L24 OR L25 OR L26 OR L27
L33          53 S L28 OR L29 OR L30 OR L31 OR L32
L34          50 S L33 NOT 2011/PY
L35          43 S L34 NOT 2010/PY
L36          42 S L35 NOT 2009/PY
L37          37 S L36 NOT 2008/PY
L38          36 S L37 NOT 2007/PY
L39          33 S L38 NOT 2006/PY
L40          30 S L39 NOT 2005/PY
L41          24 S L40 NOT 2004/PY

=> log y
COST IN U.S. DOLLARS                        SINCE FILE        TOTAL
                                              ENTRY     SESSION
FULL ESTIMATED COST                            864.32      865.01

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)          SINCE FILE        TOTAL
                                                      ENTRY     SESSION
CA SUBSCRIBER PRICE                                  -20.88      -20.88

STN INTERNATIONAL LOGOFF AT 17:00:21 ON 25 SEP 2011
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